

Sequence Listing.txt
SEQUENCE LISTING

<110> JAPAN SCIENCE AND TECHNOLOGY AGENCY

<120> Glucose and/or fructose transporter 'NaGLT1' and gene thereof

<130> 4439-4034

<140> TBA

<141> TBA

<150> JP P2002-363014

<151> 2002-12-13

<160> 30

<170> PatentIn Ver. 2.1

<210> 1

<211> 2173

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<222> (111)..(1562)

<400> 1

aaagaatctt ctggttagaa agaactgggg ctcagagctc cagggaccct ggcaaaaagc 60

tggacctcac caaaaaccct ttgtctggag ccaccaagct ggggtcggaa atg gag 116
Met Glu
1ttc cgt ggg tcc ggg gcc act gct gtt gag cag cac ctc ctc cag tcc 164
Phe Arg Gly Ser Gly Ala Thr Ala Val Glu Gln His Leu Leu Gln Ser
5 10 15gag acc cca ggg aag aat ggg ctg cag gcc aca tcg agt gac caa gtg 212
Glu Thr Pro Gly Lys Asn Gly Leu Gln Ala Thr Ser Ser Asp Gln Val
20 25 30gga aga aca ctg cgc tgg ttc acc act gtg gtt ctg aat gct gct ttc 260
Gly Arg Thr Leu Arg Trp Phe Thr Thr Val Val Leu Asn Ala Ala Phe
35 40 45 50ctg gga atg gga gtg agc gct gct gtg ctg gga ccc aca ttt cca gac 308
Leu Gly Met Gly Val Ser Ala Ala Val Leu Gly Pro Thr Phe Pro Asp
55 60 65ctg gcc aga aac gtg aac cgg aac atc agc agc ctt tcc gaa atc ttc 356
Leu Ala Arg Asn Val Asn Arg Asn Ile Ser Ser Leu Ser Glu Ile Phe
70 75 80gtg ggc cga gcc ctc ggc tac ctg ggc ggc tct gtg gtt ggt ggg gtg 404
Val Gly Arg Ala Leu Gly Tyr Leu Gly Gly Ser Val Val Gly Gly Val
85 90 95ctt ttc gac tgc atg aat cat ttt cta ctt ttg ggg ctg tcc cac ctg 452
Leu Phe Asp Cys Met Asn His Phe Leu Leu Leu Gly Leu Ser His Leu
100 105 110ctt act gcg gcc ggt ctt tac ctc act cct ttc tgt aaa aca gct gcc 500
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Sequence Listing.txt																
Leu 115	Thr	Ala	Ala	Gly	Leu 120	Tyr	Leu	Thr	Pro	Phe 125	Cys	Lys	Thr	Ala	Ala 130	
tta	ctg	act	gcc	atg	atg	tct	att	acc	ggg	gtc	tca	ttt	ggg	gtt	ctg	548
Leu	Leu	Thr	Ala	Met	Met	Ser	Ile	Thr	Gly	Val	Ser	Phe	Gly	Val	Leu	
				135					140					145		
gat	aca	ggg	ggg	aat	gtc	ctc	atc	ttg	gac	ctt	tgg	ggg	gac	aaa	gga	596
Asp	Thr	Gly	Gly	Asn	Val	Leu	Ile	Leu	Asp	Leu	Trp	Gly	Asp	Lys	Gly	
			150					155					160			
gcc	cca	cat	att	cag	gcc	ttg	cac	ttc	agt	ttc	gcc	ttg	ggg	gcc	ttc	644
Ala	Pro	His	Ile	Gln	Ala	Leu	His	Phe	Ser	Phe	Ala	Leu	Gly	Ala	Phe	
		165					170					175				
ctg	gct	ccc	ctg	ctg	gct	aaa	ttg	gcc	tgg	ggg	acc	aca	gca	tct	gct	692
Leu	Ala	Pro	Leu	Leu	Ala	Lys	Leu	Ala	Trp	Gly	Thr	Thr	Ala	Ser	Ala	
	180					185					190					
cag	aac	cac	aca	gag	cct	cag	tta	gac	cgt	tca	gcc	ttg	aac	cga	tcc	740
Gln	Asn	His	Thr	Glu	Pro	Gln	Leu	Asp	Arg	Ser	Ala	Leu	Asn	Arg	Ser	
195					200				205						210	
ttt	gaa	gcc	gcc	tca	gac	tct	gtg	ttg	gcg	gta	cct	gac	gac	atg	aat	788
Phe	Glu	Ala	Ala	Ser	Asp	Ser	Val	Leu	Ala	Val	Pro	Asp	Asp	Met	Asn	
				215					220					225		
ctt	ctg	tgg	gcg	tac	gct	tcc	att	gga	acc	tat	gtt	cta	gta	ctt	tct	836
Leu	Leu	Trp	Ala	Tyr	Ala	Ser	Ile	Gly	Thr	Tyr	Val	Leu	Val	Leu	Ser	
			230					235					240			
gtc	ttc	ctg	ttt	gct	cca	ttc	ttt	aaa	aag	agg	tca	aag	cag	aaa	aaa	884
Val	Phe	Leu	Phe	Ala	Pro	Phe	Phe	Lys	Lys	Arg	Ser	Lys	Gln	Lys	Lys	
		245					250					255				
tcc	gca	gcg	tct	gct	cag	gga	gct	cga	agg	gct	aaa	tac	cac	agg	gcc	932
Ser	Ala	Ala	Ser	Ala	Gln	Gly	Ala	Arg	Arg	Ala	Lys	Tyr	His	Arg	Ala	
	260					265					270					
ctg	cta	tgc	ctc	ctc	ttc	ctc	ttc	ttc	ttc	ttc	tac	gtg	gga	gcg	gag	980
Leu	Leu	Cys	Leu	Leu	Phe	Leu	Phe	Phe	Phe	Phe	Tyr	Val	Gly	Ala	Glu	
275					280					285					290	
gtg	acc	tac	ggc	tct	tac	gta	ttc	tcc	ttc	gcc	acc	acc	cac	gtt	ggc	1028
Val	Thr	Tyr	Gly	Ser	Tyr	Val	Phe	Ser	Phe	Ala	Thr	Thr	His	Val	Gly	
				295					300					305		
atg	gaa	gag	agc	gag	gca	gct	ggc	ttg	aac	tcc	atc	ttc	tgg	ggg	acc	1076
Met	Glu	Glu	Ser	Glu	Ala	Ala	Gly	Leu	Asn	Ser	Ile	Phe	Trp	Gly	Thr	
			310					315					320			
ttc	gca	gcc	tgc	agg	ggc	ctg	gcc	atc	ttc	ttc	gca	acg	ctc	tta	cag	1124
Phe	Ala	Ala	Cys	Arg	Gly	Leu	Ala	Ile	Phe	Phe	Ala	Thr	Leu	Leu	Gln	
		325					330					335				
cct	ggg	acc	atg	atg	gtg	ttg	tgt	aac	att	ggc	agc	ctg	gcc	tca	tct	1172
Pro	Gly	Thr	Met	Met	Val	Leu	Cys	Asn	Ile	Gly	Ser	Leu	Ala	Ser	Ser	
	340					345					350					
ttc	ttt	ctg	gtg	ctt	ttt	gac	aag	agc	cct	ctt	tgc	ctc	tgg	atc	gcg	1220
Phe	Phe	Leu	Val	Leu	Phe	Asp	Lys	Ser	Pro	Leu	Cys	Leu	Trp	Ile	Ala	
355					360					365					370	

Sequence Listing.txt

tct tct gtg tat gga gcc tca atg gct gcc acg ttt ccc agc ggc atc	1268
Ser Ser Val Tyr Gly Ala Ser Met Ala Ala Thr Phe Pro Ser Gly Ile	
375 380 385	
tcc tgg att gag cag tac acc acc tta act ggg aaa tcc gct gcg ttc	1316
Ser Trp Ile Glu Gln Tyr Thr Thr Leu Thr Gly Lys Ser Ala Ala Phe	
390 395 400	
att ctg gtt ggt gct gcc ctg gga cta atg gcg act cct gca tta tct	1364
Ile Leu Val Gly Ala Ala Leu Gly Leu Met Ala Thr Pro Ala Leu Ser	
405 410 415	
gga att ctt cag gga cac tat ccc gat ctg cca gta att ctg tac atg	1412
Gly Ile Leu Gln Gly His Tyr Pro Asp Leu Pro Val Ile Leu Tyr Met	
420 425 430	
tgt ctg ggc tca gca gta tta aca act gtg tta ttc cct gtg atg tat	1460
Cys Leu Gly Ser Ala Val Leu Thr Thr Val Leu Phe Pro Val Met Tyr	
435 440 445 450	
aaa gta gcc acc tta cct ctg gat cga aag cag gaa aaa agc atc aac	1508
Lys Val Ala Thr Leu Pro Leu Asp Arg Lys Gln Glu Lys Ser Ile Asn	
455 460 465	
agt gag ggc cag aaa ata tta ctt tct agc tct agg cta atc aag gaa	1556
Ser Glu Gly Gln Lys Ile Leu Leu Ser Ser Ser Arg Leu Ile Lys Glu	
470 475 480	
gct aaa tgaaagagga aggggaaagg tgtgaaagca cgtgcgcgcg tgtgtgcgca	1612
Ala Lys	
tgcacgcgca cgcgtaatgg ttttgcggtg gttaaaatga agaatgggac attcttcta	1672
aaaaatacaaa tagaaatgcc tttatataaac ccatagctga ggtctctaag caactctcct	1732
gaaatattct gcagccaggg tcttctccag ctgacaggga gcacgcagtc atgaggcacc	1792
aggtctcctg agaccctta cactgccctc attgaagtta tctctcagcc catgattcta	1852
ggaaagaaaa gtatttctaa aataaaatcc acgacttcca gagatcctgt aagacagctc	1912
tgagagatca atgtaactgc cagcaccttc ttcatttcca tgaagtgaga cacagaacag	1972
aaatagtttt aaacgtatgc tcctggggct ggtgagatgg cttagtggtt aagagcactg	2032
actgctcttc caaaggtcct gagttcaaata cccagcaacc acatggtggc tcacaactat	2092
ctgtaatgag atctgatgcc ttcttctggt gtgtctgaag acagcgacag tgtactcata	2152
tacatcaaataaataatatt t	2173

<210> 2
 <211> 484
 <212> PRT
 <213> Rattus norvegicus

<400> 2
 Met Glu Phe Arg Gly Ser Gly Ala Thr Ala Val Glu Gln His Leu Leu
 1 5 10 15
 Gln Ser Glu Thr Pro Gly Lys Asn Gly Leu Gln Ala Thr Ser Ser Asp
 20 25 30

Sequence Listing.txt

Gln Val Gly Arg Thr Leu Arg Trp Phe Thr Thr Val Val Leu Asn Ala
35 40 45
Ala Phe Leu Gly Met Gly Val Ser Ala Ala Val Leu Gly Pro Thr Phe
50 55 60
Pro Asp Leu Ala Arg Asn Val Asn Arg Asn Ile Ser Ser Leu Ser Glu
65 70 75 80
Ile Phe Val Gly Arg Ala Leu Gly Tyr Leu Gly Gly Ser Val Val Gly
85 90 95
Gly Val Leu Phe Asp Cys Met Asn His Phe Leu Leu Leu Gly Leu Ser
100 105 110
His Leu Leu Thr Ala Ala Gly Leu Tyr Leu Thr Pro Phe Cys Lys Thr
115 120 125
Ala Ala Leu Leu Thr Ala Met Met Ser Ile Thr Gly Val Ser Phe Gly
130 135 140
Val Leu Asp Thr Gly Gly Asn Val Leu Ile Leu Asp Leu Trp Gly Asp
145 150 155 160
Lys Gly Ala Pro His Ile Gln Ala Leu His Phe Ser Phe Ala Leu Gly
165 170 175
Ala Phe Leu Ala Pro Leu Leu Ala Lys Leu Ala Trp Gly Thr Thr Ala
180 185 190
Ser Ala Gln Asn His Thr Glu Pro Gln Leu Asp Arg Ser Ala Leu Asn
195 200 205
Arg Ser Phe Glu Ala Ala Ser Asp Ser Val Leu Ala Val Pro Asp Asp
210 215 220
Met Asn Leu Leu Trp Ala Tyr Ala Ser Ile Gly Thr Tyr Val Leu Val
225 230 235 240
Leu Ser Val Phe Leu Phe Ala Pro Phe Phe Lys Lys Arg Ser Lys Gln
245 250 255
Lys Lys Ser Ala Ala Ser Ala Gln Gly Ala Arg Arg Ala Lys Tyr His
260 265 270
Arg Ala Leu Leu Cys Leu Leu Phe Leu Phe Phe Phe Phe Tyr Val Gly
275 280 285
Ala Glu Val Thr Tyr Gly Ser Tyr Val Phe Ser Phe Ala Thr Thr His
290 295 300
Val Gly Met Glu Glu Ser Glu Ala Ala Gly Leu Asn Ser Ile Phe Trp
305 310 315 320
Gly Thr Phe Ala Ala Cys Arg Gly Leu Ala Ile Phe Phe Ala Thr Leu
325 330 335
Leu Gln Pro Gly Thr Met Met Val Leu Cys Asn Ile Gly Ser Leu Ala
340 345 350
Ser Ser Phe Phe Leu Val Leu Phe Asp Lys Ser Pro Leu Cys Leu Trp
355 360 365

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Ile Ala Ser Ser Val Tyr Gly Ala Ser Met Ala Ala Thr Phe Pro Ser
370 375 380
Gly Ile Ser Trp Ile Glu Gln Tyr Thr Thr Leu Thr Gly Lys Ser Ala
385 390 395 400
Ala Phe Ile Leu Val Gly Ala Ala Leu Gly Leu Met Ala Thr Pro Ala
405 410 415
Leu Ser Gly Ile Leu Gln Gly His Tyr Pro Asp Leu Pro Val Ile Leu
420 425 430
Tyr Met Cys Leu Gly Ser Ala Val Leu Thr Thr Val Leu Phe Pro Val
435 440 445
Met Tyr Lys Val Ala Thr Leu Pro Leu Asp Arg Lys Gln Glu Lys Ser
450 455 460
Ile Asn Ser Glu Gly Gln Lys Ile Leu Leu Ser Ser Ser Arg Leu Ile
465 470 475 480
Lys Glu Ala Lys

<210> 3
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:T3-1 forward
primer

<400> 3
tcggaaatgg agttccgtgg 20

<210> 4
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
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primer

<400> 4
agctgcctta ctgactgcca tg 22

<210> 5
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
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primer

<400> 5
tacgtattct ccttcgccac c 21

Sequence Listing.txt

<210> 6
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:T3-4 forward primer

<400> 6
tgtgtaacat tggcagcctg g 21

<210> 7
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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<400> 7
taacccatag ctgaggtctc 20

<210> 8
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:T7-1 reverse primer

<400> 8
cagatagttg tgagccacca tgtg 24

<210> 9
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:T7-2 reverse primer

<400> 9
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<220>
<223> Description of Artificial Sequence:T7-3 reverse primer

Sequence Listing.txt

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<210> 11 <211> 22 <212> DNA <213> Artificial Sequence	
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<400> 11 tctgaggcgg cttcaaagga tc	22
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<400> 12 aaaagcaccc caccaaccac ag	22
<210> 13 <211> 20 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence:NaGLT1 sense primer	
<400> 13 tgggacccac atttccagac	20
<210> 14 <211> 22 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence:NaGLT1 antisense primer	
<400> 14 tctgaggcgg cttcaaagga tc	22
<210> 15 <211> 22 <212> DNA <213> Artificial Sequence	
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Sequence Listing.txt

sense primer

<400> 15
atggacagta gcaccttgag cc 22

<210> 16
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
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antisense primer

<400> 16
tagccccaga gaagatgtct gc 22

<210> 17
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
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primer

<400> 17
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<210> 18
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
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antisense primer

<400> 18
ggacactgcc acaatgaaca cc 22

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Rat GAPDH sense
primer

<400> 19
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<210> 20
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Sequence Listing.txt

<220>
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<400> 20
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<210> 21
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<220>
 <223> Description of Artificial Sequence:NaGLT1 forward primer

<400> 21
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<210> 22
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<220>
 <223> Description of Artificial Sequence:NaGLT1 reverse primer

<400> 22
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<210> 23
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<220>
 <223> Description of Artificial Sequence:NaGLT1 TaqMan probe

<400> 23
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<210> 24
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<220>
 <223> Description of Artificial Sequence:Rat SGLT1 forward primer

<400> 24
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<210> 25
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Sequence Listing.txt

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Rat SGLT1
reverse primer

<400> 25
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<210> 26
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Rat SGLT1
TaqMan probe

<400> 26
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<210> 27
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Rat SGLT2
forward primer

<400> 27
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<210> 28
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Rat SGLT2
reverse primer

<400> 28
gacaaattgg ccaccatctt g 21

<210> 29
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Rat SGLT2
TaqMan probe

<400> 29
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<210> 30

Sequence Listing.txt

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:NaGLT1
C-terminal peptide

<400> 30

Leu Pro Leu Asp Arg Lys Gln Glu Lys Ser Ile Asn Ser Glu Gly Gln
1 5 10 15